

FORM PTO-1449

U. S DEPARTMENT OF COMMERCE  
PATENT AND TRADEMARK OFFICE

ATTY. DOCKET NO.

SERIAL NO.

U 012911-3

09/643,407

INFORMATION DISCLOSURE  
STATEMENT BY APPLICANT

(Use several sheets if necessary)



APPLICANT

Itzhak PEER, et al.

FILING DATE

GROUP

August 22, 2000

1643

## REFERENCE DESIGNATION

## U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB-CLASS	FILING DATE IF APPROPRIATE
AA							
AB							
AC							
AD							
AE							
AF							
AG							
AH							
AI							
AJ							
AK							

RECEIVED

DEC 20 2001

TECH CENTER 1600/2900

## FOREIGN PATENT DOCUMENTS

	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB-CLASS	TRANSLATION
						YES
AL						
AM						
AN						
AO						
AP						

## OTHER ART (Including Author, Title, Date, Pertinent Dates, Etc.)

GSM	AR	PE'ER,I. ET AL. "SPECTRUM ALIGNMENT: EFFICIENT RESEQUENCING BY HYBRIDIZATION"
		PROCESSING OF THIS 8 <sup>TH</sup> INTERNATIONAL CONFERENCE ON INTELLIGENT SYSTEMS FOR
	AS	MOLECULAR BIOLOGY (ISMB) (2000) PP 1-9 ✓
	AT	

EXAMINER

*O. Malt*

DATE CONSIDERED

*1/12/02*

EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

FORM PTO-1449 U. S DEPARTMENT OF COMMERCE  
PATENT AND TRADEMARK OFFICE

INFORMATION DISCLOSURE  
STATEMENT BY APPLICANT

(Use several sheets if necessary)

ATTY. DOCKET NO.	SERIAL NO.
U 012911-3	09/643,407
APPLICANT	
Itzhak PEER, et al.	
FILING DATE	GROUP
August 22, 2000	1643

REFERENCE DESIGNATION

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER						DATE	NAME	CLASS	SUB-CLASS	FILING DATE IF APPROPRIATE
CGM	AA	5	4	9	2	8	0	6	2/1996	Drmanac	435	6
CGM	AB	5	5	2	5	4	6	4	6/1996	Drmanac	435	6
CGM	AC	5	6	6	7	9	7	2	9/1997	Drmanac	435	6
CGM	AD	5	6	9	5	9	4	0	12/1997	Drmanac	536	23

FOREIGN PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB-CLASS	TRANSLATION	
							YES	NO
CGM	AE	9 0 0 4 6 2 5	10/1989	WO	—	—	X	

OTHER ART (Including Author, Title, Date, Pertinent Dates, Etc.)

CGM	✓ AF	Bains, W., et al. "A Novel Method for Nucleic Acid Sequence Determination" <i>J. Theor. Biol.</i> , Vol. 135, p. 303-307, (1988)
CGM	✓ AG	Ben-Dor, A., et al. "On the Complexity of Postional Sequencing by Hybridization" <i>Proc. 10<sup>th</sup> Int'l. Conf. On Combinatorial Pattern Matching (CPM '99)</i> , p. 88-100, (1999)
CGM	✓ AH	Cargill, M., et al. "Characterization of single-nucleotide polymorphisms in coding regions of human genes" <i>Nature Genetics</i> , Vol. 22, p. 231-238, (1999)
CGM	✓ AI	Durbin, R., et al. "Biological Sequence Analysis: Probabilisitic models of proteins and nucleic acids" Cambridge University Press, (1998)
CGM	✓ AJ	Eddy, S.R. "Hidden Markov models" <i>Current Opinions in Structural Biology</i> , Vol. 6, No. 3, p. 361-365, (1996)
CGM	✓ AK	Hirschberg, D.S. "A Linear Space Algorithm for Computing Maximal Common Subsequences" <i>Communications of the ACM</i> , Vol. 18, No. 6, p. 341-343, (1975)
CGM	✓ AL	Jukes, T.H., et al. "Evolutionary Change in Nucleotide Sequences" <i>Mammalian Protein Metabolism</i> , New York, Academic Press, p. 21-123, (1969)
CGM	✓ AM	Khrapko, K.R., et al. "Oligonucleotide hybridization approach to DNA sequencing" <i>FEBS Letters</i> , Vol. 256, p. 118-122, (1989)
CGM	✓ AN	Kimura, M. "A Simple Method for Estimating Evolutionary Rates of Base...Nucleotide Sequences", <i>J. Mol. Evol.</i> , Vol. 16, p. 111-120, (1980)

EXAMINER

*C. Ma TC*

DATE CONSIDERED

*1/12/02*

EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

FORM PTO-1449

U. S DEPARTMENT OF COMMERCE  
PATENT AND TRADEMARK OFFICEINFORMATION DISCLOSURE  
STATEMENT BY APPLICANT

(Use several sheets if necessary)

ATTY. DOCKET NO.	SERIAL NO.
U 012911-3	09/643,407
APPLICANT	
Itzhak PEER, et al.	
FILING DATE	GROUP
August 22, 2000	1643

## REFERENCE DESIGNATION

## U.S. PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUB-CLASS	FILING DATE IF APPROPRIATE
AA						
OTHER ART (Including Author, Title, Date, Pertinent Dates, Etc.)						
<i>DEC 12 2001</i> CIP E JC68 USPTO PATENT & TRADEMARK OFFICE ✓ Krogh, A., et al. "Hidden Markov Models in Computational Biology: Applications to Protein Modeling UCSC-CRL-93-32" Dept. of Computer and Information Sciences, UCSC, (1993)						
AC ✓ Krogh, A., et al. "Hidden Markov Models in Computational Biology: Applications to Protein Modeling" <i>J. Mol. Biol.</i> , Vol. 235, p. 1501-1531, (1994)						
✓ AD ✓ Lysov, Y.P., et al. "Determining DNA Nucleotide Sequence by Means of Oligonucleotides Hybridization: A New Method" <i>Dokl. Acad. Sci.</i> , USSR, Vol. 303, p. 1508-1511, (1988)						
✓ AE ✓ Pevzner, P.A., et al. "Towards DNA Sequencing Chips" <i>Mathematical Foundations of Computer Science, LNCS</i> , Vol. 841, p. 143-158, (1994)						
✓ AF ✓ Pevzner, P.A., et al. "Improved Chips for Sequencing by Hybridization" <i>J. Biomol. Struct. Dyn.</i> , Vol. 9, No. 2, (1991)						
✓ AG ✓ Frieze, A.M., et al. "Optimal Reconstruction of a Sequence from its Probes" <i>Journal of Computational Biology</i> , Vol. 6, No. 3/4, p. 361-368, (1999)						
✓ AH ✓ Skiena, S.S., et al. "Reconstructing Strings from Substrings" <i>Journal of Computational Biology</i> , Vol. 2, No. 2, p. 333-353, (1995)						
✓ AI ✓ Smith, T.F., et al. "Identification of Common Molecular Subsequences" <i>J. Mol. Biol.</i> , Vol. 147, p. 195-197, (1981)						
✓ AJ ✓ Southern, E.M., et al. "Analyzing and Comparing Nucleic Acid Sequences by Hybridization to Arrays of ...Experimental Models" <i>Genomics</i> , Vol. 13, p. 1008-1017, (1992)						
✓ AK ✓ Southern, E.M. "DNA Chips: Analysing Sequence by Hybridization to Oligonucleotides on a Large Scale" <i>Trends in Genetics</i> , Vol. 12, p. 110-115, (1996)						
✓ AL ✓ Wang, D.G., et al. "Large-Scale Identification, Mapping, and Genotyping of Single-Nucleotide Polymorphisms...Genome" <i>Science</i> , Vol. 280, p. 1077-1082, (1998)						
✓ AM ✓ Yang, Z. "Maximum-Likelihood Estimation of Phylogeny from DNA Sequences When Substitution Rates Differ over Sites" <i>Molecular Biology and Evolution</i> , Vol. 10, p. 1396-1401, (1993)						

EXAMINER

*C.-M.L.*

DATE CONSIDERED

*1/12/02*

EXAMINER:

Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.